

# Sequencing the Bad Guys

**A** high-tech piece of equipment, hard work, and collaboration have brought researchers a few steps closer to developing new tests and vaccines for several troublesome cattle diseases.

Scientists at ARS' Bacterial Diseases of Livestock Research Unit in Ames, Iowa, and the University of Minnesota (U-M) have sequenced the chromosomes of two disease-causing microbes—those that cause Johne's disease and bovine brucellosis—and have moved into the finishing phase of work on an agent that brings about leptospirosis. That project is being done completely within the ARS unit, which is part of the National Animal Disease Center (NADC).

The arrival at Ames of a DNA sequence analyzer has made much of this work possible. "Our sequencing capacity was a limiting factor for large-scale projects," says ARS veterinary medical officer David Alt, who operates the analyzer. "Now we can perform almost 800 reactions a day." The sequencer can automatically analyze multiple runs of 96 DNA samples, making unattended 24-hour operation possible.

Alt compares a sequenced genome to a book. "We can read the book from start to finish," he says. "We are not going to understand every word in it, but it's a starting point that may lead to treatments, vaccines, and diagnostic means that are better than those currently available."

Automated sequencing allows for rapid analysis of an organism's genes, speeding identification of those linked to superior characteristics or to negative traits such as susceptibility to disease. Scientists and breeders can then, theoretically, root out or exploit specific genes to breed improved varieties or

species. The Ames/U-M research seeks to identify genes that are associated with disease and that show potential in vaccine development.

NADC's first sequencing project was on *Mycobacterium paratuberculosis*. That microbe causes Johne's disease, an intestinal disorder characterized by diarrhea and weight loss in infected cattle and found in 7 percent of beef herds and 22 percent of dairy herds nationwide. ARS microbiologist John Bannantine

important public health concern.—By **Luis Pons**, ARS.

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**Microbial** causes of some livestock diseases are among the latest organisms to be genetically mapped.

and Vivek Kapur, a U-M pathogenomics scientist, led this research.

"With the sequencing," says Bannantine, "we hope to understand the biology of *M. paratuberculosis*, identify unique disease-causing genes, and—most importantly—develop new diagnostic tests."

ARS microbiologist Shirley Halling led sequencing work on *Brucella abortus*, which causes bovine brucellosis. This highly contagious bacterial disease induces late-term abortions and infertility in cows. It can also bring about undulant fever in humans.

The sequencing of *Leptospira borgpetersenii* serovar *hardjo*, a cause of leptospirosis, is being led by ARS microbiologist Richard Zuerner. Leptospirosis causes abortions, stillbirths, and weak offspring in cattle and swine and can reduce milk production in cows. It also affects many other animals, including dogs, and is an

The maps are a starting point that may lead to treatments, vaccines, and diagnostic means for Johne's disease and bovine brucellosis.